

Organization Applicant

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 <110> OrganizationName : Amylin Pharmaceuticals, Inc.

Application Project

 <120> Title : TREATMENT OF PANCREATITIS WITH AMYLIN
 <130> AppFileReference : 0101-UTL-0
 <140> CurrentAppNumber :
 <141> CurrentFilingDate : 24 September 2003

Sequence

 <213> OrganismName : human
 <400> PreSequenceString :
 KCNTATCATQ RLANFLVHSS NNFGAILSST NVGSNTY 37
 <212> Type : PRT
 <211> Length : 37
 SequenceName : 1
 SequenceDescription :

Sequence

 <213> OrganismName : Artificial Sequence
 <400> PreSequenceString :
 XXNTATXATQ RLXNFLXXXX XNXGXXLXXT XVGSNTY 37
 <212> Type : PRT
 <211> Length : 37
 SequenceName : 2
 SequenceDescription :

Feature

 Sequence: 2:
 <221> FeatureKey : MOD_RES
 <222> LocationFrom : 1
 <222> LocationTo : 1
 Other Information : X is Lys, Ala, Ser or hydrogen
 CDSJoin : No

Feature

 Sequence: 2:
 <221> FeatureKey : MOD_RES
 <222> LocationFrom : 2
 <222> LocationTo : 2
 Other Information : X at position 2 and X at position 7 are independently
 selected amino acid residues having side chains which are chemically bonded to each
 other to form an intramolecular linkage
 CDSJoin : No

Feature

 Sequence: 2:
 <221> FeatureKey : MOD_RES

<222> LocationFrom : 7
<222> LocationTo : 7
Other Information : X at position 2 and X at position 7 are independently
selected amino acid residues having side chains which are chemically bonded to each
other to form an intramolecular linkage
CDSJoin : No

Feature

Sequence: 2:
<221> FeatureKey : MOD_RES
<222> LocationFrom : 13
<222> LocationTo : 13
Other Information : X is Ala, Ser or Thr
CDSJoin : No

Feature

Sequence: 2:
<221> FeatureKey : MOD_RES
<222> LocationFrom : 17
<222> LocationTo : 17
Other Information : X is Val, Leu or Ile
CDSJoin : No

Feature

Sequence: 2:
<221> FeatureKey : MOD_RES
<222> LocationFrom : 18
<222> LocationTo : 18
Other Information : X is His or Arg
CDSJoin : No

Feature

Sequence: 2:
<221> FeatureKey : MOD_RES
<222> LocationFrom : 19
<222> LocationTo : 19
Other Information : X is Ser or Thr
CDSJoin : No

Feature

Sequence: 2:
<221> FeatureKey : MOD_RES
<222> LocationFrom : 20
<222> LocationTo : 20
Other Information : X is Ser, Thr, Gln or Asn
CDSJoin : No

Feature

Sequence: 2:
<221> FeatureKey : MOD_RES
<222> LocationFrom : 21
<222> LocationTo : 21
Other Information : X is Asn, Gln or His
CDSJoin : No

Feature

Sequence: 2:
<221> FeatureKey : MOD_RES
<222> LocationFrom : 23
<222> LocationTo : 23
Other Information : X is Phe, Leu or Tyr
CDSJoin : No

Feature

Sequence: 2:
<221> FeatureKey : MOD_RES
<222> LocationFrom : 25
<222> LocationTo : 25
Other Information : X is Ala or Pro
CDSJoin : No

Feature

Sequence: 2:
<221> FeatureKey : MOD_RES
<222> LocationFrom : 26
<222> LocationTo : 26
Other Information : X is Ile, Val, Ala or Leu
CDSJoin : No

Feature

Sequence: 2:
<221> FeatureKey : MOD_RES
<222> LocationFrom : 28
<222> LocationTo : 28
Other Information : X is Ser, Pro, Leu, Ile or Thr
CDSJoin : No

Feature

Sequence: 2:
<221> FeatureKey : MOD_RES
<222> LocationFrom : 29
<222> LocationTo : 29
Other Information : X is Ser, Pro or Thr
CDSJoin : No

Feature

Sequence: 2:
<221> FeatureKey : MOD_RES
<222> LocationFrom : 31
<222> LocationTo : 31
Other Information : X is Asn, Asp, or Gln
CDSJoin : No